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Figure 20 (part a) shows a threading alignment of interleukin-1 β (IL-1 β SEQ ID NO:6) and FGF-2 (FGF2 SEQ ID NO:7) used for homology modeling. Insertions are indicated by dashes. The bars above and below the alignment show the beta strand positions in interleukin-1 β (above) and FGF-2 (below) as defined in the PDB structure files. The sequence alignment identity is 12.7%. Figure 18 (part b) also shows DALI structural alignment of IL-1 β and FGF-2. The structural root-mean-square deviation (RMSD) of the DALI alignment is 2.7 Å over 101 residues.

REMARKS

The amendment is made in adherence with rules 37 C.F.R. §1.821-1.825. This amendment is accompanied by a floppy disc containing SEQUENCE ID NUMBERS 1-7 in computer readable form, and a paper copy of the sequence information. The information contained in the computer readable disc is identical to that of the paper copy. This amendment contains no new matter. Applicants submit that this amendment, the accompanying computer readable sequence listing, and the paper copy thereof serve to place this application in a condition of adherence to the rules of rules 37 C.F.R. §1.821-1.825.

Applicants believe that all pending claims are allowable and respectfully requests a Notice of Allowance for this application from the Examiner. Should the Examiner believe that a telephone conference would expedite the prosecution of this application, the undersigned can be reached at the telephone number set out below.

Respectfully submitted,

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Marked-Up Version Showing Changes Made

Figure 18 is a MALDI-TOF PSD spectrum of crosslinked peptide $MH^+ = m/z$ 2739.4 arising from peptides Tyr73-Lys86 (**SEQ ID NO:1**) linked to Thr 121-Lys129 (**SEQ ID NO:2**).

Figures 19A and 19B are MALDI-TOF spectra of intra-molecular crosslinked peptide (**SEQ ID NO:3**) at $MH^+ = m/z$ 2059 (A) and intermolecular crosslinked peptide (**SEQ ID NO:4**) and (**SEQ ID NO:5**) at $MH^+ = m/z$ 2565 (B).

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